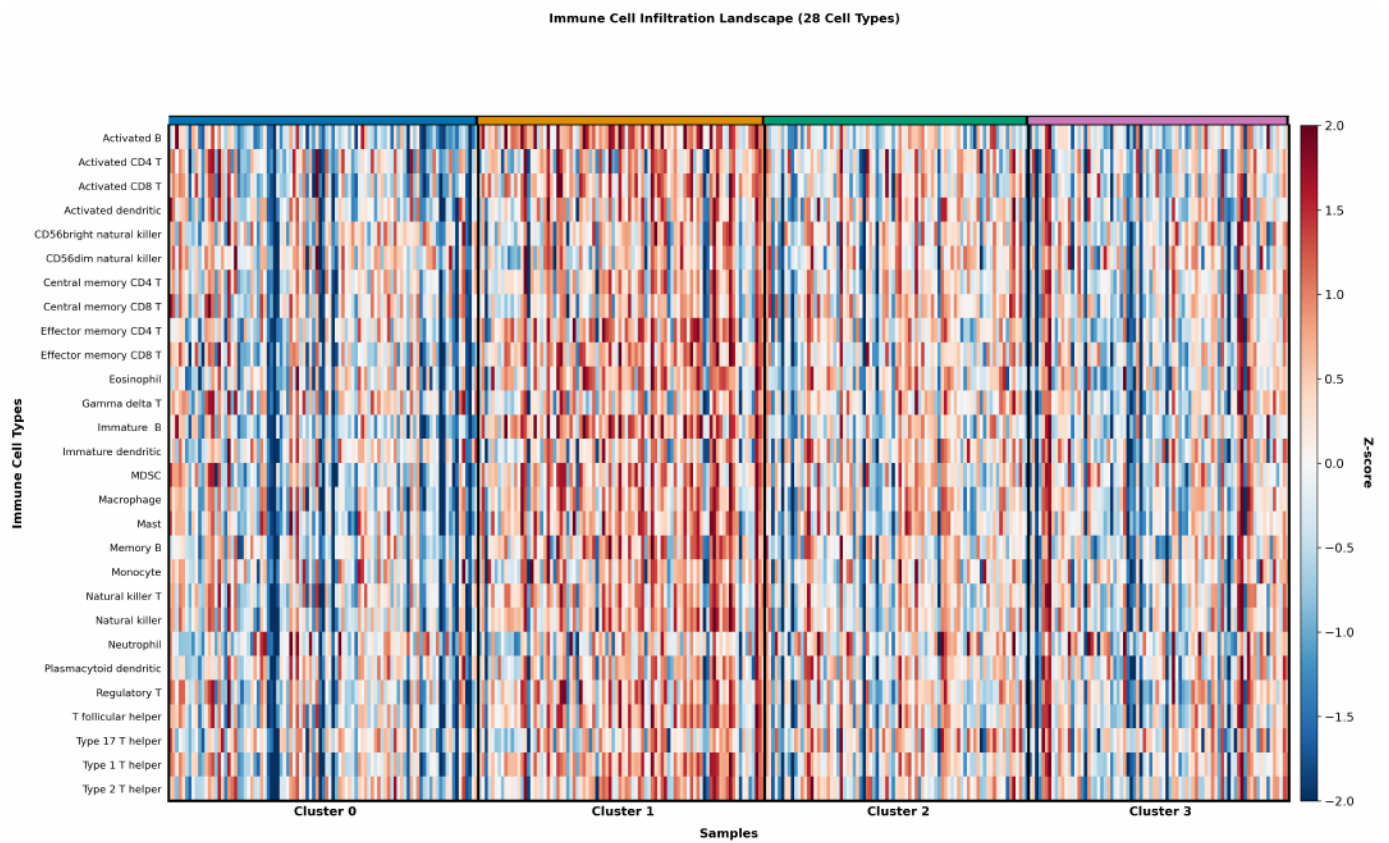
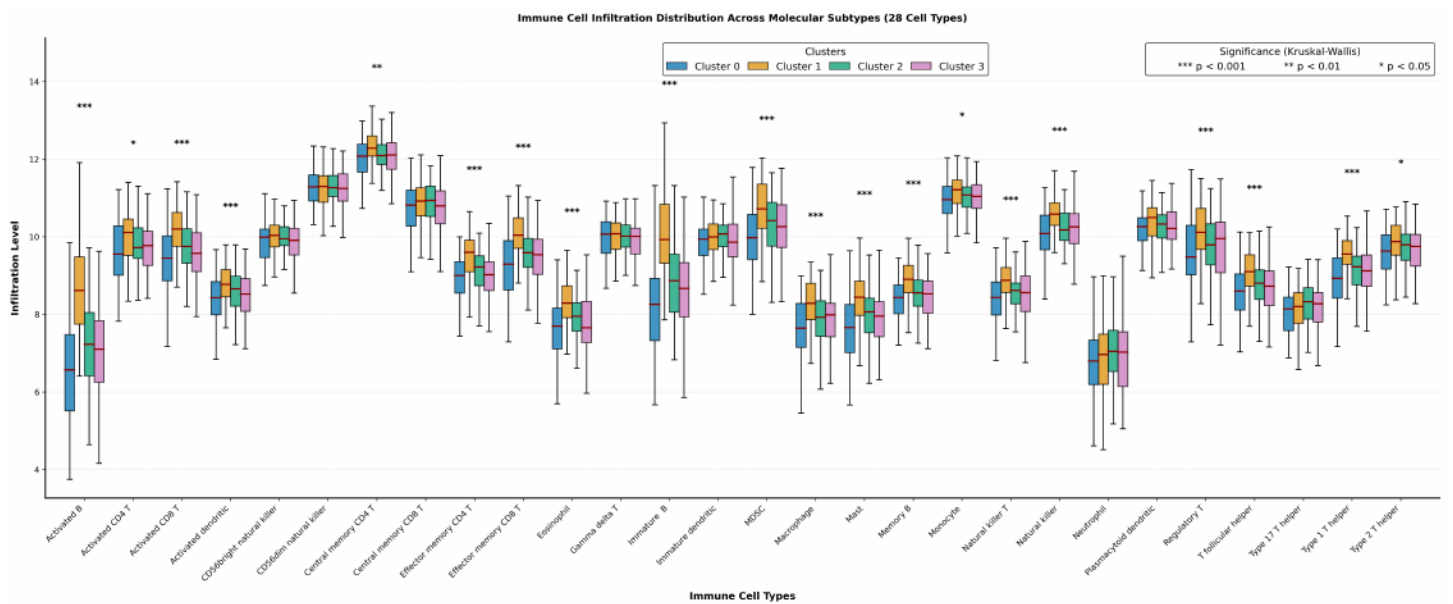


a



b

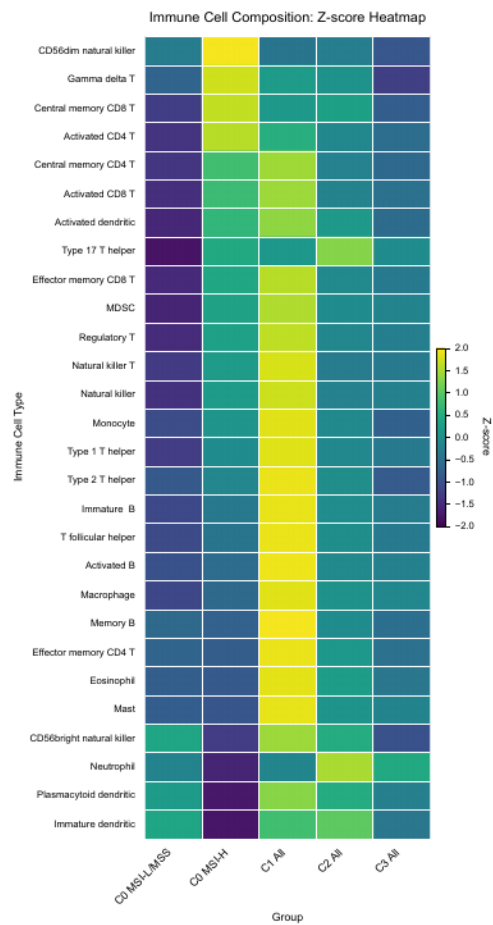


Extended Data Fig. 1 | Immune cell infiltration landscape and inter-cluster differences across mACE subtypes.

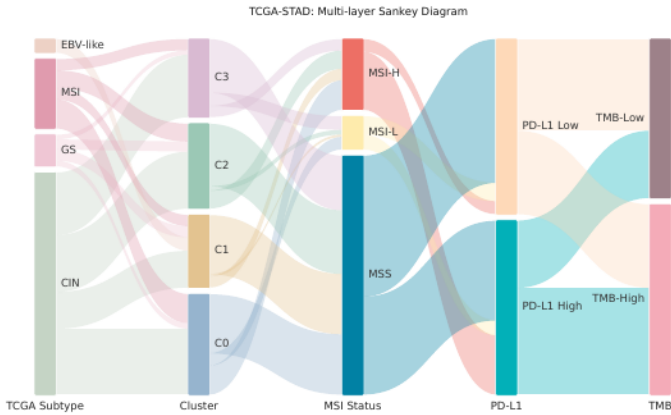
a, Heatmap of Z-scored ssGSEA enrichment scores for 28 immune cell types across all TCGA-STAD samples (n = 336), ordered by mACE cluster assignment (C0-C3). Colour scale represents row Z-score ranging from -2.0 (blue) to +2.0 (red).

b, Boxplots comparing infiltration levels of all 28 immune cell types across the four mACE clusters. Centre line, median; box limits, IQR; whiskers, 1.5x IQR. Statistical significance assessed by Kruskal-Wallis test (***P < 0.001, **P < 0.01, *P < 0.05).

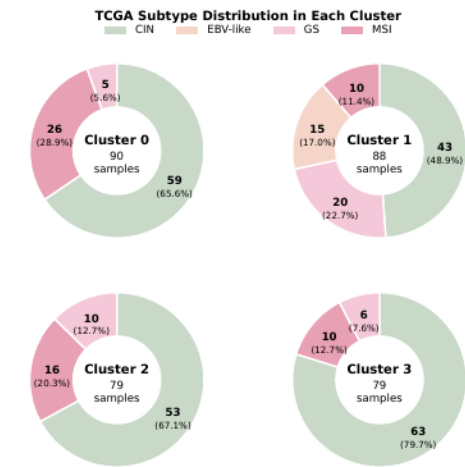
a



b



c



Extended Data Fig. 2 | Molecular subtype distribution and biomarker landscape across mACE immune subtypes.

a, Z-score heatmap of 28 immune cell type abundances stratified by MSI status within Cluster 0 (C0 MSI-L/MSS and C0 MSI-H) and overall immune composition across C1, C2, and C3.

b, Multi-layer Sankey diagram depicting patient flow from TCGA molecular subtype (EBV-like, MSI, GS, CIN) through mACE cluster assignment to MSI status, PD-L1 expression, and TMB classification across the TCGA-STAD cohort (n = 336).

c, Donut charts showing the proportional distribution of TCGA molecular subtypes within each mACE cluster (C0, n = 90; C1, n = 88; C2, n = 79; C3, n = 79). Numbers indicate sample counts and percentages.